

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is primate DIRS1 nucleotide sequence.
SEQ ID NO: 2 is primate DIRS1 polypeptide sequence.
SEQ ID NO: 3 is primate DIRS2 nucleotide sequence.
SEQ ID NO: 4 is primate DIRS2 polypeptide sequence.
SEQ ID NO: 5 is primate IFNY receptor subunit beta polypeptide sequence.
10 SEQ ID NO: 6 is primate CRF2-4 receptor subunit polypeptide sequence.

(1) GENERAL INFORMATION:

15 (i) APPLICANT: Parham, Christi L.
Moore, Kevin W.
Murgolo, Nicholas J.
Bazan, J. Fernando

20 (ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related
Reagents and Methods

(iii) NUMBER OF SEQUENCES: 6

25 (iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
35 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

40 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 08-MAR-1999
(C) CLASSIFICATION:

45 (viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0804K

50 (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1381 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- 10 (B) LOCATION: 132..1064

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 567
- 15 (D) OTHER INFORMATION: /note= "nucleotides 567, 573, 1336, 1342, and 1369 designated C, but each may be A, C, G, or T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 20 (B) LOCATION: 643
- (D) OTHER INFORMATION: /note= "nucleotides 643, 1287, and 1290 designated C, but each may be C or G"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 772
- 25 (D) OTHER INFORMATION: /note= "nucleotides 772, 806, and 1261 designated G, but each may be A or G"

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1236
- (D) OTHER INFORMATION: /note= "nucleotides 1236, 1260, 1282, and 1289 are designated T, but each may be G or T"

35 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1247
- 40 (D) OTHER INFORMATION: /note= "nucleotides 1247, 1257, 1293, and 1302 designated C, but each may be C or T"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1266
- 45 (D) OTHER INFORMATION: /note= "nucleotides 1266 and 1298 designated T, but each may be A or T"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACCCACG CGTCCGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA	60
AGATGGCTGA GATGGACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAAC	120
55 GAGTCTACCA A ATG CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA	170

	Met Gln Thr Phe Thr Met Val Leu Glu Ile Trp Thr			
	1	5	10	
5	AGT CTT TTC ATG TGG TTT TTC TAC GCA TTG ATT CCA TGT TTG CTC ACA Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr 15 20 25			218
10	GAT GAA GTG GCC ATT CTG CCT GCC CCT CAG AAC CTC TCT GTA CTC TCA Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser 30 35 40 45			266
15	ACC AAC ATG AAG CAT CTC TTG ATG TGG AGC CCA GTG ATC GCG CCT GGA Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly 50 55 60			314
20	GAA ACA GTG TAC TAT TCT GTC GAA TAC CAG GGG GAG TAC GAG AGC CTG Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu 65 70 75			362
25	TAC ACG AGC CAC ATC TGG ATC CCC AGC AGC TGG TGC TCA CTC ACT GAA Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu 80 85 90			410
30	GGT CCT GAG TGT GAT GTC ACT GAT GAC ATC ACG GCC ACT GTG CCA TAC Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr 95 100 105			458
35	AAC CTT CGT GTC AGG GCC ACA TTG GGC TCA CAG ACC TCA GCC TGG AGC Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser 110 115 120 125			506
40	ATC CTG AAG CAT CCC TTT AAT AGA AAC TCA ACC ATC CTT ACC CGA CCT Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro 130 135 140			554
45	GGG ATG GAG ATC CCC AAA CAT GGC TTC CAC CTG GTT ATT GAG CTG GAG Gly Met Glu Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu 145 150 155			602
50	GAC CTG GGG CCC CAG TTT GAG TTC CTT GTG GCC TAC TGG ACG AGG GAG Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu 160 165 170			650
55	CCT GGT GCC GAG GAA CAT GTC AAA ATG GTG AGG AGT GGG GGT ATT CCA Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro 175 180 185			698
60	GTG CAC CTA GAA ACC ATG GAG CCA GGG GCT GCA TAC TGT GTG AAG GCC Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala 190 195 200 205			746
65	CAG ACA TTC GTG AAG GCC ATT GGG AGG TAC AGC GCC TTC AGC CAG ACA Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr 210 215 220			794

	GAA TGT GTG GAG GTG CAA GGA GAG GGC ATT CCC CTG GTA CTG GCC CTG Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu 225 230 235	842
5	TTT GCC TTT GTT GGC TTC ATG CTG ATC CTT GTG GTC GTG CCA CTG TTC Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe 240 245 250	890
10	GTC TGG AAA ATG GGC CGG CTG CTC CAG TAC TCC TGT TGC CCC GTG GTG Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val 255 260 265	938
15	GTC CTC CCA GAC ACC TTG AAA ATA ACC AAT TCA CCC CAG AAG TTA ATC Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile 270 275 280 285	986
20	AGC TGC AGA AGG GAG GAG GTG GAT GCC TGT GCC ACG GCT GTG ATG TCT Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser 290 295 300	1034
	CCT GAG GAA CTC CTC AGG GCC TGG ATC TCA TAGGTTTGCG GAAGGGCCCA Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser 305 310	1084
25	GGTGAAGCCG AGAACCTGGT CTGCATGACA TGGAAACCAT GAGGGGACAA GTTGTGTTTC TGTGTTCCGC CACGGACAAG GGATGAGAGA AGTAGGAAGA GCCTGTTGTC TACAAGTCTA GAAGCAACCA TCAGAGGCAG GGTGGTTGT CTAACAGAAC AACTGACTGA GGCTATGGGG 30	1144
	GTTGTGACCT CTAGACTTTG GGCTTCCACT TGCTTGGCTG AGCAACCCTG GGAAAAGTGA CTTCATCCCT TCGGTCCCAA GTTTCTCAT CTGTAATGGG GGATCCCTAC AAAACTG	1204
35	(2) INFORMATION FOR SEQ ID NO:2:	1264

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe 1 5 10 15
50	Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val 20 25 30
	Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met 35 40 45

	Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val			
	50	55	60	
	Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser			
5	65	70	75	80
	His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu			
	85	90	95	
10	Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg			
	100	105	110	
	Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys			
	115	120	125	
15	His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu			
	130	135	140	
20	Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly			
	145	150	155	160
	Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu Pro Gly Ala			
	165	170	175	
25	Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu			
	180	185	190	
	Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe			
	195	200	205	
30	Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val			
	210	215	220	
35	Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe			
	225	230	235	240
	Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys			
	245	250	255	
40	Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro			
	260	265	270	
	Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg			
	275	280	285	
45	Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu			
	290	295	300	
50	Leu Leu Arg Ala Trp Ile Ser			
	305	310		

(2) INFORMATION FOR SEQ ID NO:3:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1244 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- 10 (B) LOCATION: 2..694

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 193
- 15 (D) OTHER INFORMATION: /note= "nucleotide 193 designated C, may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	C CGG GTC GAC CCA CGC GTC CGC CTG GTT TCC CCC TGG CTG ACA GTG Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val 1 5 10 15	46
25	CCT TGG TTC CTG TCC TGT TGG AAT GTT ACC ATT GGG CCT CCT GAG AGC Pro Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser 20 25 30	94
30	ATC TGG GTG ACG CCG GGA GAA GCC TCC CTC ATC ATC AGG TTC TCC TCT Ile Trp Val Thr Pro Gly Ala Ser Leu Ile Ile Arg Phe Ser Ser 35 40 45	142
35	CCC TTC GAC GTC CCT CCC AAC CTG GGC TAT TTC CAG TAC TAT GTC CAT Pro Phe Asp Val Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His 50 55 60	190
40	TAC TGG GAA AAG GCG GGA ATC CAA AAG GTT AAA GGT CCT TTC AAG AGC Tyr Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser 65 70 75	238
45	AAC TCC ATC GTG TTG GAT GGC TTG AGA CCC TTA AGA GAA TAC TGT TTA Asn Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu 80 85 90 95	286
50	CAA GTG AAG GCG CAT CTC TTT CGC ACA TCC TGC AAC ACC TCT AGG CCC Gln Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro 100 105 110	334
55	GGC CGC TTA AGC AAC ATA ACT TGC TAC GAA ACA ATG ATG GAT GCC ACT Gly Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr 115 120 125	382
55	ACG AAG CTT CAA CAA GTC ATC CTC ATC GCC GTG GGA GTC TTT CTG TCG Thr Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser 130 135 140	430

	CTG GCG GCG CTG GCG GGG GGC TGT TTC TTC CTG GTG CTG AGA TAC AAA	478
	Leu Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys	
145	150	155
5	GGC CTG GTG AAA TAC TGG TTT CAC TCT CCG CCA AGC ATC CCA TCA CAA	526
	Gly Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln	
160	165	170
	175	
10	ATC GAA GAG TAT CTG AAG GAC CCG AGC CAG CCT ATC CTA GAG GCC CTG	574
	Ile Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu	
	180	185
	190	
15	GAC AAG GAC ACG TCA CCA ACA GAT GAT GCC TGG GAC TTG GTG TCT GTT	622
	Asp Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val	
	195	200
	205	
20	GTT GCA TTT CCA GCA AAG GAG CAA GAA GAT GTT CCC CAA AGC ACT TTG	670
	Val Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu	
	210	215
	220	
	ACC CAA AAC TCT GGT GCG GTC TGC TAGCCTGTGG GGTAAGGGCT CTGAGCCGAG	724
	Thr Gln Asn Ser Gly Ala Val Cys	
	225	230
25	GAAGCTGCTG ATGTCCATGT CAGCACTTTA TGGAATCCGG TCCTCCATTT TCCTGTCCCC	784
	AAAAGGCCCG TCAGTGCCTG TGAAGATGTA ACGGGTCTCA TGGGGCGAC AAGCTTATTG	844
30	ATTTTTTCT TCAAACTAAG AGTTTCTAA TCATACGCGT TTTTAGAATA ATTCTACAGA	904
	TATGTCCCCG AAAGATTAAG ATTTCTCTTA AACACTAAAA AGACATGTAA TTATTTGTTA	964
	GCAAATGGGC GTCTGGCACG CCTCTGACAC TTTTCGTCA GCAGCCAGGA CACGAGGTCC	1024
35	CCTCCTTGAT GAAGCCCCTC GGGCAGACCA TGTCACCTGT CCCAGCCTGC CCCAAGAAGG	1084
	GACATTAAGT GGCCCTTCTT CATATCCAAA CACCTGGCTT GAAATGTGAT TAGCCCTGTA	1144
40	AATAGTTCTA CAGAGATTAAG GCCTTTTTT CCCCCAAGTT AGGAATAAAA GACTATAATT	1204
	AACTTTTAA AAAAAAAA AAAAAAAA AAAAAAAA	1244

45 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Arg	Val	Asp	Pro	Arg	Val	Arg	Leu	Val	Ser	Pro	Trp	Leu	Thr	Val	Pro				
1																15				
	5																			
5	Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	Ile				
																30				
	20																			
	35	Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro			
																45				
10	50	Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Tyr			
	55	65	Trp	Glu	Lys	Ala	Gly	Ile	Gln	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn			
																80				
15	70	85	Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln		
																95				
	100	105	110	Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly	
20																				
	115	120	125	Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr	
25	130	135	140	Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu	
	145	150	155	160	Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly
30																				
	165	170	175	Leu	Val	Lys	Tyr	Trp	Phe	His	Ser	Pro	Pro	Ser	Ile	Pro	Ser	Gln	Ile	
35	180	185	190	Glu	Glu	Tyr	Leu	Lys	Asp	Pro	Ser	Gln	Pro	Ile	Leu	Glu	Ala	Leu	Asp	
	195	200	205	Lys	Asp	Thr	Ser	Pro	Thr	Asp	Asp	Ala	Trp	Asp	Leu	Val	Ser	Val	Val	
40	210	215	220	Ala	Phe	Pro	Ala	Lys	Glu	Gln	Glu	Asp	Val	Pro	Gln	Ser	Thr	Leu	Thr	
	225	230	Gln	Asn	Ser	Gly	Ala	Val	Cys											
45																				
	(2)	INFORMATION FOR SEQ ID NO:5:																		

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe
1 5 10 15

10 Ala Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
20 25 30

15 Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
35 40 45

20 Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg
50 55 60

25 Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
65 70 75 80

30 Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
85 90 95

35 Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
100 105 110

40 Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
115 120 125

45 Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
130 135 140

50 Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
145 150 155 160

55 Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
165 170 175

60 Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
180 185 190

65 Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
195 200 205

70 Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
210 215 220

75 Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
225 230 235 240

80 Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
245 250 255

85 Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
275 280 285

5 Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
305 310 315 320

10 Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
325 330 335

Leu

15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

35 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

40 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

45 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

50 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
115 120 125

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140

5 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175

10 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
195 200 205

15 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala
210 215 220

20 Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
225 230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe
245 250 255

25 Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His
260 265 270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu
275 280 285

30 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser
290 295 300

35 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly
305 310 315 320

Gln Gly Pro Gln Ser
325